BIOTEC OLOGY
SYSTEMS
BRANCH

RECEIVED
SEP 0 7 2001
TECH CENTER 1600/2900

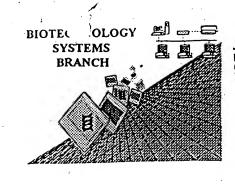# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/218,913C

Source: 1652

Date Processed by STIC: 7/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: US/09/218,913C   TIME: 13:25:21

Input Set : A:\98,736.SEQ.LST.txt
Output Set: N:\CRF3\07202001\I218913C.raw

```
   3 <110> APPLICANT: Hall, Roderick L
   4         Poll, Christopher T.
   5         Newton, Benjamin B.
   6         Taylor, William J.A.
   8 <120> TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance
   9 <130> FILE REFERENCE: 98,736
  11 <140> CURRENT APPLICATION NUMBER: 09/218,913C
  12 <141> CURRENT FILING DATE: 1998-12-22
  14 <160> NUMBER OF SEQ ID NOS: 71
  16 <170> SOFTWARE: Microsoft Word 97
```

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

```
 332 <210> SEQ ID NO: 11
 333 <211> LENGTH: (170)
 334 <212> TYPE: PRT
 335 <213> ORGANISM: Homo sapien
 337 <220> FEATURE:
 338 <221> NAME/KEY: peptide
 339 <222> LOCATION: 1..170
 340 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 21-26, 40, 42, 45-47, 52,
 64,
 341         103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any
 342         amino acid residue"
 344 <400> SEQUENCE: 11
 345 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val
 346 1                   5                   10                  15
 348 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
 349           20                  25                  30
 351 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser
 352         35                  40                  45
 354 Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa
 355     50                  55                  60
 357 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 358 65                  70                  75                  80
 360 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 361             85                  90                  95
 363 Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa
 364             100                 105                 110
 366 Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
 367         115                 120                 125
 369 Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn
 370     130                 135                 140
 372 Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln
 373 145                 150                 155                 160
 375 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 376             165                 170                 175
```

Length shown as 170 but actual length is 179 (see next page)

```
E--> 378 Ala Val Ser  ⓒ-179
    537 <210> SEQ ID NO: 16
    538 <211> LENGTH: (428)  — Length Listed as 428, actual
    539 <212> TYPE: DNA                 length is 431
    540 <213> ORGANISM: Homo sapien
    542 <220> FEATURE:
    543 <221> NAME/KEY: misc_feature
    544 <222> LOCATION: 1..430
    545 <223> OTHER INFORMATION: /note= "n at positions 3, 11, 12, 17, 51 and 429 represent
any nucleic acid"
    547 <400> SEQUENCE: 16
W--> 548 gcngcgcgtt nntcgcntgc tgggatcgct gctgcacctc tctggggtcg nggcggccga    60
    550 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc   120
    552 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg   180
    554 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc   240
    556 cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc   300
    558 tgtcccaagt gctcccagaa ggcaggattc ttgaagacca cttcagcgat atgttcaact   360
    560 atgaagaata ctggcaccgc caacgcattc actgggcctg cgtgcatcct tcccacgctg   420
E--> 562 gtactttgnc g                                                       (431)
    893 <210> SEQ ID NO: 35
    894 <211> LENGTH: (36)  —— Length differs              (37)
    895 <212> TYPE: DNA
    896 <213> ORGANISM: Homo sapien
    898 <400> SEQUENCE: 35
E--> 899 ggtctagagg ccgggtcgtt tctcgcctgg ctggga
   1396 <210> SEQ ID NO: 54
   1397 <211> LENGTH: 23
   1398 <212> TYPE: DNA
   1399 <213> ORGANISM: Homo sapien
   1401 <220> FEATURE:
   1402 <223> OTHER INFORMATION: Human Bikunin protein fragment
   1404 <400> SEQUENCE: 54
   1405 Met Leu Arg Ala Glu Ala Asp Gly Asn Ser Arg Leu Leu Gly Ser Leu
   1406 1               5                   10                  15
   1408 Leu Leu Ser Gly Val Leu Ala
B--> 1409             20
   1515 <210> SEQ ID NO: 64
   1516 <211> LENGTH: (20)  — Length differs
   1517 <212> TYPE: PRT
   1518 <213> ORGANISM: Homo sapien
   1520 <220> FEATURE:
   1521 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"
   1523 <400> SEQUENCE: 64
   1524 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
   1525 1               5                   10                  15
   1527 Val Gly Arg (Cys) -21
E--> 1528            20
   1668 <210> SEQ ID NO: 71
   1669 <211> LENGTH: 225
   1670 <212> TYPE: PRT
```

RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: US/09/218,913C   TIME: 13:25:21

Input Set : A:\98,736.SEQ.LST.txt
Output Set: N:\CRF3\07202001\I218913C.raw

```
1671 <213> ORGANISM: Homo sapien
1673 <220> FEATURE:
1674 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"
1676 <400> SEQUENCE: 71
1677 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1678 1               5                   10                  15
1680 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
1681             20                  25                  30
1683 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
1684             35                  40                  45
1686 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
1687         50                  55                  60
1689 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
1690 65                  70                  75                  80
1692 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
1693             85                  90                  95
1695 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
1696             100                 105                 110
1698 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
1699             115                 120                 125
1701 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
1702         130                 135                 140
1704 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
1705 145                 150                 155                 160
1707 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
1708             165                 170                 175
1710 Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
1711             180                 185                 190
1713 Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
1714         195                 200                 205
1716 Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
1717         210                 215                 220
1719 Leu
1720 225
E--> 1725 ⓘ
```

(handwritten) remove miscellaneous material at the end of file

VERIFICATION SUMMARY   DATE: 07/20/2001
PATENT APPLICATION: US/09/218,913C   TIME: 13:25:22

Input Set : **A:\98,736.SEQ.LST.txt**
Output Set: **N:\CRF3\07202001\I218913C.raw**

```
L:9 M:283 W: Missing Blank Line separator, <130> field identifier
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:378 M:252 E: No. of Seq. differs, <211>LENGTH:Input:170 Found:179 SEQ:11
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:426 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:562 M:252 E: No. of Seq. differs, <211>LENGTH:Input:428 Found:431 SEQ:16
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:597 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:899 M:254 E: No. of Bases conflict, LENGTH:Input:37 Counted:36 SEQ:35
L:991 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:1098 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:1205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:1409 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:0 SEQ:54
L:1528 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:64
L:1725 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:71
```